

Database version 5.1.4  
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Sequence search, using SW model

From: 279, 2002, 17:58:46 Search Time: 509 Seconds

(with all parameters)  
11874.137 Millions cell updates/sec

Database: 09-715-983-1

Sequence: 1 Parameter: 1 Parameter: 1 Parameter: 1 Parameter: 1 Parameter: 1

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10 1541.6 45.4 1861 21 AA546144

11 1240.6 46.5 10464 22 AA137338

12 648.2 19.2 5783 17 AA112246

13 627.8 18.6 902 22 AA194068

14 604.2 17.9 4121 22 AA511807

15 576.8 17.1 777 22 AA196007

16 571.4 16.9 792 22 AA196006

17 514.8 15.3 647 22 AA528471

18 419.6 12.4 2840 22 AA586169

19 374 11.7 604 22 AA570403

20 374 11.1 604 22 AA570403

21 282.8 8.4 764 20 AA539794

22 258 7.7 2208 24 AA502094

23 246.8 7.3 446 21 AA046011

24 217 6.4 422 22 AA199335

25 184 5.5 5946 22 AA137340

26 144.2 4.0 797 22 AA199726

27 88.8 2.6 4215 23 AA105045

28 88.8 2.6 7941 23 AA105044

29 80.4 2.4 216 20 AA197943

30 67.8 2.0 6485 22 AA546159

31 67.8 2.0 6485 24 AA138008

32 64.2 1.9 6608 24 AA138007

33 63.2 1.9 6419 24 AA132487

34 62.8 1.9 6644 20 AA533181

35 62.8 1.9 7372 20 AA533182

36 62.8 1.9 7797 20 AA533180

37 62.8 1.9 7996 20 AA533184

38 62.2 1.8 14006 24 AA139058

39 61 1.8 6109 24 AA139056

40 61 1.8 6109 24 AA139057

41 60.8 1.8 6145 24 AA132972

42 58.6 1.8 7291 24 AA132927

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AA546144

AA137338

AA112246

AA194068

AA511807

AA196007

AA196006

AA528471

AA586169

AA570403

AA570403

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AA502094

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AA199335

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AA105044

AA197943

AA546159

AA138008

AA138007

AA132487

AA533181

AA533182

AA533180

AA533184

AA139058

AA139056

AA139057

AA132972

AA132927

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XX 14-SRP-1995.  
 XX 13-MAR-1995; 95MO-0S03385.  
 XX 11-MAR-1994; 94US-0208887.  
 XX (UNYV) UNIV NEW YORK STATE.

XX Marolis BL, Schlesinger J, Skolnik EY;  
 DR WP1: 1995-128245/42.  
 XX P-PSUB: AAR85784.

PT DNA encoding tyrosine kinase binding proteins - used to screen  
 PT agents capable of modulating cell growth or cellular metabolism

XX **Example 3: Page 125-127; 215pp; English.**

CC Using a new cloning technique, c-Kit (cloning of receptor targets)  
 CC several new tyrosine kinase (TK) binding proteins were isolated. Growth  
 CC factor receptor bound proteins (Grb-1, Grb-2, Grb-3, Grb-4, Grb-7 and  
 CC Grb-10) were isolated using this method. This sequence encodes Grb-1.  
 CC The proteins bind to a tyrosine phosphorylated domain of a catalytic  
 CC TK. Grb proteins can be used for screening agents which are capable  
 CC of modulating cell growth that occurs via signal transduction through  
 CC TKs. Such agents can be used to prevent or inhibit cell growth or to  
 CC counteract tumour development. Grb proteins are also useful for  
 CC identifying susceptibility to diseases associated with alterations in  
 CC cellular metabolism mediated by TK pathways e.g. cancer and diabetes.  
 XX Sequence 4372 BP: 1110 A: 661 C: 716 G: 885 T: 0 other:

Query Match 99.6%; Score 3457.6; DB 16; Length 3372;  
 Best Local Similarity 99.7%; Pred No 0;  
 Matches 3363; Conservative 0; Mismatches 9; Indels 0; Caps 0;

QY 1 TCAACACAGGCTCAACCTGTCATGCTAGCAGATTGGCAACAGACGTCGTAGGCGGTAC 60  
 DB 1 TCAACACAGGCTCAACCTGTCATGCTAGCAGATTGGCAACAGACGTCGTAGGCGGTAC 60  
 QY 61 CATTAT 120  
 DB 61 CATTAT 120  
 QY 121 GGTGACATATGACTGCTATATATATATATATATATATATATATATATATATATAT 180  
 DB 121 GGTGACATATGACTGCTATATATATATATATATATATATATATATATATATATAT 180  
 QY 181 GAAGCTAGAGCTGGAACAAATTTGGTCTTAAATGCTATATATATATATATATATAT 240  
 DB 181 GAAGCTAGAGCTGGAACAAATTTGGTCTTAAATGCTATATATATATATATATATAT 240  
 QY 241 GAGGACATTTGCTTAAATGCTATATATATATATATATATATATATATATATATAT 300  
 DB 241 GAGGACATTTGCTTAAATGCTATATATATATATATATATATATATATATATATAT 300  
 QY 301 GATTAAT 360  
 DB 301 GATTAAT 360  
 QY 361 GATTTGATGACAGCAATTTGATATATATATATATATATATATATATATATATATAT 420  
 DB 361 GATTTGATGACAGCAATTTGATATATATATATATATATATATATATATATATATAT 420  
 QY 421 ATTGACACCTGCTCTTAT 480  
 DB 421 ATTGACACCTGCTCTTAT 480  
 QY 481 TCAATCTATATAGAGACAGAGCTTCAGCAACCTGGAGCAATATAGCAACAGCTTTGAT 540  
 DB 481 TCAATCTATATAGAGACAGAGCTTCAGCAACCTGGAGCAATATAGCAACAGCTTTGAT 540

QY 541 TCGTATATACCCCTGCTGATGCTGAGATATGAGATATGCTATATGCTGATGCTTTC 600  
 DB 541 TCGTATATACCCCTGCTGATGCTGAGATATGAGATATGCTATATGCTGATGCTTTC 600  
 QY 601 AAAGCTATCTCTCTGAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGATGCT 660  
 DB 601 AAAGCTATCTCTCTGAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGATGCT 660  
 QY 661 ATTCTTATGCTGAGCAAT 720  
 DB 661 ATTCTTATGCTGAGCAAT 720  
 QY 721 ATTGATGCTGAGCAAT 780  
 DB 721 ATTGATGCTGAGCAAT 780  
 QY 781 TCTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 840  
 DB 781 TCTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 840  
 QY 841 ATTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 900  
 DB 841 ATTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 900  
 QY 901 ATTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 960  
 DB 901 ATTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 960  
 QY 961 ATTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 1020  
 DB 961 ATTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 1020  
 QY 1021 TCTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 1080  
 DB 1021 TCTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 1080  
 QY 1081 CTTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 1140  
 DB 1081 CTTTCACAGCTTCTTCACAGCTTACCAATGCTCTGATATGCTGATGCTGATGCTGAT 1140  
 QY 1141 GATTAAT 1200  
 DB 1141 GATTAAT 1200  
 QY 1201 GATTAAT 1260  
 DB 1201 GATTAAT 1260  
 QY 1261 GATTAAT 1320  
 DB 1261 GATTAAT 1320  
 QY 1321 GATTAAT 1380  
 DB 1321 GATTAAT 1380  
 QY 1381 GATTAAT 1440  
 DB 1381 GATTAAT 1440  
 QY 1441 GATTAAT 1500  
 DB 1441 GATTAAT 1500  
 QY 1501 GATTAAT 1560  
 DB 1501 GATTAAT 1560  
 QY 1561 GATTAAT 1620  
 DB 1561 GATTAAT 1620  
 QY 1621 AATTAT 1680  
 DB 1621 AATTAT 1680



XX 05-MAY-1997: 9705-0850993.  
 XX (NOVO) NOVO-NORDISK AS.  
 PA Andersen CB, Hansen T, Pedersen OB;  
 XX WPI: 1999-539565/45.  
 XX  
 PT Altered nucleic acids encoding p85alpha subunits of human  
 PT phosphatidylinositol 3-kinase, useful for identifying mutations that  
 PT may be associated with impaired glucose transport and metabolism  
 PS  
 PS Disclosure: Columns 3-4; 14pp; English.

CC The present sequence encodes the regulatory p85-alpha subunit of human  
 CC phosphatidylinositol 3-kinase (PI3K). PI3K binds to growth factor plasma  
 CC membrane receptors (including insulin receptors) and signaling motifs in  
 CC signaling proteins and modulates the activity of these molecules through  
 CC tyrosine kinase activity. It is also associated with vesicle trafficking  
 CC and protein sorting and therefore acts as a mediator of insulin action on  
 CC glucose transport and metabolism. The specification describes a mutated  
 CC p85-alpha nucleic acid sequence which comprises the mutations relative  
 CC to the present sequence: C261T, T66G, A810G, and/or G1020A. The nucleic  
 CC acids may be used to detect mutated genes encoding the p85 alpha subunit  
 CC of PI3K and to identify mutations which may alter the activity of the  
 CC protein. PI3K is associated with  
 CC processes, membrane ruffling, actin reorganization in K5 cells in  
 CC response to insulin, protein sorting and in membrane and vesicle  
 CC trafficking. Therefore, PI3K acts as a mediator of insulin action on  
 CC glucose transport and metabolism. Mutations in the PI3K gene result in  
 CC decreased glucose disappearance rates, decreased glucose effectiveness  
 CC and decreased glucose sensitivity. Consequently, mutations in PI3K genes  
 CC are associated with glucose resistance or (impaired glucose tolerance),  
 CC non-insulin dependent diabetes mellitus (NIDDM), cardiovascular disease,  
 CC obesity and hypertension and other diseases resulting from altered  
 CC glucose metabolism.

XX  
 XX Sequence 2508 bp: 833 A; 520 C; 538 G; 617 T; 0 other;

Query Match 73.8%; Score 248.6; DB 20; Length 2508;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2504; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 1 TACAACTCAAGTCACTGTTATGCTATACAGATTGCTAAATATGATGCTGAGAGGATAC 60  
 DB 1 TACAACTCAAGTCACTGTTATGCTATACAGATTGCTAAATATGATGCTGAGAGGATAC 60  
 QY 61 CACTACAGAGGCTGATGATTAATAAAGGAAAGAGAGAGATGATGATGCTGCTG 120  
 DB 61 CACTACAGAGGCTGATGATTAATAAAGGAAAGAGAGAGATGATGATGCTGCTG 120  
 QY 121 GTGATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 DB 121 GTGATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 QY 181 GAAGTCAAGTCTGAGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 DB 181 GAAGTCAAGTCTGAGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 241 GGGGATTTGGGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 DB 241 GGGGATTTGGGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 QY 301 GCAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 DB 301 GCAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 QY 361 GATGTTGAATCAAGAGCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 DB 361 GATGTTGAATCAAGAGCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 ATGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 DB 421 ATGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 QY 481 TCACTTATACAGACACACAGCTGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 DB 481 TCACTTATACAGACACACAGCTGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 QY 541 TGTGATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 DB 541 TGTGATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 QY 601 AAAGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 DB 601 AAAGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 661 ATTTCTTACGCTGAGAGTATCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 DB 661 ATTTCTTACGCTGAGAGTATCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 QY 721 ATTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 DB 721 ATTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 QY 781 TCTTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
 DB 781 TCTTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
 QY 841 ATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 DB 841 ATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 QY 901 ATTAAGTATATGAAATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 DB 901 ATTAAGTATATGAAATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 QY 961 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 DB 961 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 QY 1021 TCTTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 DB 1021 TCTTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 QY 1081 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 DB 1081 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 QY 1141 GATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
 DB 1141 GATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
 QY 1201 GATGCGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 DB 1201 GATGCGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 QY 1261 GATGCGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
 DB 1261 GATGCGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
 QY 1321 GATGCGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
 DB 1321 GATGCGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
 QY 1381 AAAAATTAATGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
 DB 1381 AAAAATTAATGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
 QY 1441 TATGAAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
 DB 1441 TATGAAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
 QY 1501 TTTAATGAACCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 DB 1501 TTTAATGAACCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560



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QY 1013 ACAATAGTCTACAAAATGCGAATGCTACTGGGACATATCTCAGGAAATGTA 1072  
DB 210 ACAATAGTCTACAAAATGCGAATGCTACTGGGACATATCTCAGGAAATGTA 269  
QY 1073 ATAAAAACCTTGAGATACAGCAGACGAGCTTTTGGTAAAGAGATGGTACTAAAA 1132  
DB 270 ATAAAAACCTTGAGATACAGCAGACGAGCTTTTGGTAAAGAGATGGTACTAAAA 329  
QY 1133 TGGATGGATATATCTCTTACACTAAGGAAAGGGGAAATACAAATTAACAAAATAT 1192  
DB 330 TGGATGGATATATCTCTTACACTAAGGAAAGGGGAAATTAATTAATCAAAAATAT 389  
QY 1193 TTGATGAAATGAGAAATATGCTTCTGTGACCTTAACCTTTCAGTCTGTGGTGAAT 1252  
DB 390 TTGATGAAATATGAGAAATATGCTTCTGTGACCTTAACCTTTCAGTCTGTGGTGAAT 449  
QY 1253 TAATAACCACTACCGGAAATGCAATCTAGTCTAGTATATCTGAAATGCAATGAAAT 1312  
DB 450 TAATAACCACTACCGGAAATGCAATCTAGTCTAGTATATCTGAAATGCAATGAAAT 509  
QY 1313 TATTTATGCAATATGCAATATGCAACAGGATGAGTGGTGAACAAATATATTAAG 1372  
DB 510 TATTTATGCAATATGCAATATGCAACAGGATGAGTGGTGAACAAATATATTAAG 569  
QY 1373 CTGTAGGAAAAAATTCATGATATACACACAGTTCACAGAAAAAGTGGAGATATG 1432  
DB 570 CTGTAGGAAAAAATTCATGATATACACACAGTTCACAGAAAAAGTGGAGATATG 629  
QY 1433 ATAGATATATGAGAAATATACCTGCTACCTGAGGAAATCTAAATGAAAGGACAGCTA 1492  
DB 630 ATAGATATATGAGAAATATACCTGCTACCTGAGGAAATCTAAATGAAAGGACAGCTA 689  
QY 1493 TTGAACTATTATGAAACCAATAAATAATATGAAAGAAAGTGGGACAGGAGAGGCT 1552  
DB 690 TTGAACTATTATGAAACCAATAAATAATATGAAAGAAAGTGGGACAGGAGAGGCT 749  
QY 1553 ACAGGAAAGAAATACATGAAAGAAATTTAAAGGAGAAAGTAAATGAAAGAAATGAAAGG 1612  
DB 750 ACAGGAAAGAAATACATGAAAGAAATTTAAAGGAGAAAGTAAATGAAAGAAATGAAAGG 809  
QY 1613 TTATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1672  
DB 810 TTATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 869  
QY 1673 GATTTGAAAGAAAGTGGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1732  
DB 870 GATTTGAAAGAAAGTGGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 929  
QY 1733 ATAGCAATTAAGCAAGCTTATGCAAGCTGAAAGCAAGCAAGCAAGCAAGCAAGCAAG 1792  
DB 930 ATAGCAATTAAGCAAGCTTATGCAAGCTGAAAGCAAGCAAGCAAGCAAGCAAGCAAG 989  
QY 1793 TACCTTAAAAAGTGTGGGAAAGGAGTGAAGCAAGTGGTGGTGAATGAAAGCAAGTGTG 1852  
DB 990 TACCTTAAAAAGTGTGGGAAAGGAGTGAAGCAAGTGGTGGTGAATGAAAGCAAGTGTG 1949  
QY 1853 AAAGCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1912  
DB 1050 AAAGCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1109  
QY 1913 GATATGTTGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 1972  
DB 1110 GATATGTTGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 1159  
QY 1973 GCACTTTCTGTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2032  
DB 1170 GCACTTTCTGTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1229  
QY 2033 ATAGCAATTAAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2092  
DB 1230 ATAGCAATTAAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1289  
QY 2093 GATATGTTGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 2152

DB 1290 GCTATACCTGTAAGCAAGTGTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 1349  
QY 2153 TGTAGCAAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2212  
DB 1350 TGTAGCAAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 1409  
QY 2213 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2272  
DB 1410 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 1469  
QY 2273 AGCAAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2332  
DB 1470 AGCAAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 1529  
QY 2333 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2392  
DB 1530 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 1589  
QY 2393 AGCAAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2452  
DB 1590 AGCAAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 1649  
QY 2453 TGTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2512  
DB 1650 TGTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1709  
QY 2513 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2572  
DB 1710 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1769  
QY 2573 GCTTACCACTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 2632  
DB 1770 GCTTACCACTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 1829  
QY 2633 GCTTACCACTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 2692  
DB 1830 GCTTACCACTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 1889  
QY 2693 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2752  
DB 1890 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 1949  
QY 2753 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2812  
DB 1950 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2009  
QY 2813 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2872  
DB 2010 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 2069  
QY 2873 AAAAATGAGTGTGAAAGCAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 2932  
DB 2070 AAAAATGAGTGTGAAAGCAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 2129  
QY 2933 ATATGAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 2992  
DB 2130 ATATGAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTGAAAGTGTG 2189  
QY 2993 TGTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3052  
DB 2190 TGTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2249  
QY 3053 TGTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3112  
DB 2250 TGTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2409  
QY 3113 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3172  
DB 2310 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2369  
QY 3173 GATGAGCAAGTGTGCTGAAAGCAAGTGTGCTGATATGAGCAAGCAAGTGTG 3232













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QY	1973	GCATTTTCCTGGTCCGGAAATGATTAAGACAGCTGCTATATCTGCTTTGTAATGCTGAT	2032
Db	1444	GCATTTTCCTGGTCCGGAAATGATTAAGACAGCTGCTATATCTGCTTTGTAATGCTGAT	1403
QY	2093	ACCGTGAAGCTAAGATATCTGCTGATAAACAAACAGTAACTATATATGCTTTTCCGAGT	2092
Db	1404	ACCGTGAAGTAAAGTATCTGCTGATTAAGCAACAGTAACTATATATGCTTTTCCGAGT	1463
QY	2093	CCCTAACTCTGATAGCTCTGCTGAAACAGCTGCTGCTATATGTAACAGCTTCCGCTTG	2152
Db	1444	CCCTAACTCTGATAGCTCTGCTGAAACAGCTGCTGCTATATGTAACAGCTTCCGCTTG	1523
QY	2153	TGCACAGCAATACAGATATGCTTAATGCTACATATACCTATACCAATATATGACAAACAT	2212
Db	1523	TGCACAGCAATACAGATATGCTTAATGCTACATATACCTATACCAATATATGACAAACAT	1584
QY	2213	GATGAGAGCGCTACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2272
Db	1584	GATGAGAGCGCTACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1643
QY	2273	ACGCAAAAGCTCTGCTCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTG	2332
Db	1644	ACGCAAAAGCTCTGCTCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTG	1703
QY	2333	CTTTGGATGGACTAAGCTTTCTTTTACACAAAAAAGAGTAAATGGAAGTATGTCAGCTTA	2392
Db	1704	TTTTGCAAGCGACATGCGCTCTCTTTGACAAAAAAGAGTAAATGGAAGTATGTCAGCTTA	1763
QY	2393	AGCGTGATATATGATGCAATCTGCTGAAGCTGAGAGCTTAAGCTTTTTCCTTTT	2452
Db	1764	AGCGTGATATATGATGCAATCTGCTGAAGCTGAGAGCTTAAGCTTTTTCCTTTT	1823
QY	2453	TCTTTGGTTAATTTTAAAGTGCAGATTCACATTCACATC	2490
Db	1823	TCTTTGGTTAATTTTAAAGTGCAGATTCACATTCACATC	1861
RESULT 11			
AAL37338			
ID	AAL37338	standard; DNA; 10494 bp.	
XX	AAL37338;		
XX	08-JAN-2000	(first entry)	
XX			
XX		Human musculoskeletal system related polypeptide like CTG ID NO. 3703.	
XX			
XX		24 Statin, immunoprotection, muscle fiber, non-specific, activity; antiallergic, hepatotoxicity, antidiabetic, antiinflammatory; antitumor; cardiovascular, antineoplastic, antidiabetic, antiparasitic; cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted proteins; musculoskeletal system; ds.	
XX			
XX		Homo sapiens.	
XX		W020015367-A1.	
XX			
XX		02-AUG-2001.	
XX			
XX		17-JAN-2001; 2001W010501338.	
XX			
XX		31-JAN-2000; 2000G05-0179065.	
XX		04-FEB-2000; 2000G05-0180628.	
XX		24-FEB-2000; 2000G05-0184664.	
XX		02-MAR-2000; 2000G05-0186350.	
XX		16-MAR-2000; 2000G05-0189874.	
XX		17-MAR-2000; 2000G05-0190876.	
XX		18-APR-2000; 2000G05-0198123.	
XX		19-MAY-2000; 2000G05-0205515.	
XX		07-JUN-2000; 2000G05-0209467.	
XX		29-JUN-2000; 2000G05-0214886.	
XX		30-JUN-2000; 2000G05-0215135.	



DB 9367 3GATTATTTCATTTTGTAACTAATGAAACCATATCTACGAAAGAAAGGCAAGCTTCCACTGACAA

[illegible][illegible]



OS Homo sapiens.  
 XX W0200166719 At.  
 XX  
 PD 13-SEP-2001.  
 XX  
 XX 02-MAR-2001: 2001WO-101620  
 PF  
 XX 07-MAR-2000: 2000JP-0166166  
 PR  
 PA (CHIR-) CHIBA PHARMACEUTICAL CO. LTD.  
 PA (HISM-) HISAMITSU PHARM CO. LTD.  
 XX  
 PI Nakagawara A.  
 XX  
 DR WPI: 2001-565584/63.  
 XX

PT Nucleic acids originating in gene expressed in human neuroblastoma,  
 PT useful as probe or primer in diagnosing prognosis of human  
 PT neuroblastoma, malignancy and susceptibility indicator of tumor marker  
 PT for anti-cancer agents.

PS Claim 1: Page 148-139; 297pp; Japanese.

CC The invention relates to novel genes (AA153926 AA157663) expressed in  
 CC human neuroblastoma. The nucleic acids are applicable as a probe or  
 CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
 CC susceptibility indicators of tumor markers for anti-cancer agents. The  
 CC gene information for diagnosis prognosis is related to Lactobacillus  
 CC to that for N-myc and TrkA genes.

XX Sequence 902 BP; 332 A; 151 C; 171 G; 217 T; 31 other;

Query Match 18.6%; Score 627.9; DB 22; Length 902;  
 Best local similarity 94.8%; Pred. Seq. 136-143;  
 Matches 699; Conservative 0; Mismatches 30; Gaps 8; Gaps 5;

QY 953 CAGCAGACATGCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1012  
 DB 170 CAGCAGACATGCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 229  
 QY 1013 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1072  
 DB 230 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 289  
 QY 1073 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1129  
 DB 290 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 349  
 QY 1130 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1189  
 DB 350 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 409  
 QY 1190 TATTTCAGAGAGATGAGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1249  
 DB 410 TATTTCAGAGATGAGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 469  
 QY 1250 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1309  
 DB 470 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 529  
 QY 1310 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1369  
 DB 530 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 589  
 QY 1370 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1429  
 DB 590 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 649  
 QY 1430 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 1489  
 DB 650 AATAATGCTCTCTCTAAACCAACCAAAAGCTACTAGTACAGCAACAGGTAAGATA 709

QY 1490 GTATTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 1549  
 DB 710 GTATTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 769  
 QY 1550 GTATTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 1609  
 DB 750 GTATTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 809  
 QY 1610 GTATTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 1669  
 DB 820 GTATTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 879  
 QY 1669 AGAAGATTTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 1719  
 DB 886 AGAAGATTTGAGGATTTATATTAACCAATTAATTTGATTAATTTGATTAATTTGATTAATTT 939

RESULT 14

AAK51887  
 ID AAK51887 standard, cDNA, 422 BP.

AC AAK51887;

DT 06-NOV-2001 (first entry)

AX Human polynucleotide SEQ ID NO 432.

DE Human cytokine cell proliferation cell differentiation gene therapy;

EM Cancer, leukemia therapy; stem cell growth factor; hematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukemia;

KW nervous system disorders; arthritis; inflammation; ss.

OS Homo sapiens.

XX W0200157199-A2.

XX 09-AUG-2001.

XX 05-FEB-2001: 2001WO-0504098.

XX 03-FEB-2000: 2000US-0496914.

XX 27-APR-2000: 2000US-0560875.

XX 20-JUN-2000: 2000US-0598075.

XX 19-JUL-2000: 2000US-0628225.

XX 01-SEP-2000: 2000US-0654930.

XX 15-SEP-2000: 2000US-0661561.

XX 20-OCT-2000: 2000US-0691325.

XX 20-NOV-2000: 2000US-0728422.

XX (HNSC-) HNSC INC.

XX Yang YL, Liu Y, Immortel K1, Asundi V, Zhou F, Xu C, Gao Y, Ma Y;

XX Zhao Q, Wang D, Wang J, Zhou F, Ren F, Chen R, Wang Z;

XX Xue AJ, Yang Y, Wejberman T, Goodrich J;

XX WPI: 2001 476282/51.

XX P-RSDB: AAK78754.

XX Nucleic acids encoding polypeptides with cytokine-like activities,

XX useful in diagnosis and gene therapy.

XX Claim 1: Page 1596 1600; 622pp; English.

CC The invention relates to polynucleotides (AAK51887-AAK51895) and the  
 CC encoded polypeptides (AAK51887-AAK51895) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation of which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have value as the active activities,  
 CC e.g. stem cell growth factor activity, hematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activity/kill in cell growth and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and



QY 2973 TGGTATGCTTGGTGGACGGCTAATATCTTATACCTGTGTGCAAAAGTGGTGTAGA 2192  
 DB 4111 GGGCTGGCGCTTGGCGAGCTCTTACAACTGTAGCGGTGGCTGAAAGGAGCTGGTGGTGA 3170  
 QY 2133 TTAACAACACACCTCCCTTGTGTAGACGACAAAGCACTCCCTGATATGTACACCTAGCTTACC 2192  
 DB 3171 GTACGACGACGCGCTGCTGTGTGACGACAAAGCACTCCCTGATATGTACACCTAGCTTACC 3240  
 QY 2193 AGTATATGTACAG 2205  
 DB 3231 AGTGGCGGCGCG 3243  
 RESULT 15  
 AA196007C  
 ID AA196007 standard: cDNA; 777 BP.  
 AC AA196007  
 AT 13-NOV-2001 (first entry)  
 DE Human neuroblast cell expressed polyomavirus PTA-802 (p. 1082).  
 EM Human, heart (tumor), malignancy, age 0-1, type 0, pathol. N myo, TKA, ss  
 OS Homo sapiens.  
 PH WC20016719 A1  
 XX 13-SEP-2001.  
 PD 02-MAR-2001; 2001WC-JP01629.  
 PF 97-MAR-2000; 2000JP-016296  
 PA (CHIB-) CHIBA PRECEPTURE.  
 PA (HISM-) HISAMITSU PHARM CO LTD.  
 PI Nakagawara A;  
 DR WP1: 2001-565584/53.  
 XX  
 PT Nucleic acids originating in gene expressed in human neuroblastoma.  
 PT useful as probe or primer in diagnosing prognosis of human  
 PI neuroblastoma, malignancy and susceptibility indicator or tumor marker  
 PT for anti-cancer agents.  
 PS Claim 1: Page 1537; 2979pp; Japanese.  
 XX  
 CC The invention relates to novel genes (AA196007, AA197963) expressed in  
 CC human neuroblastoma. The nucleic acids are applicable as a probe or  
 CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
 CC susceptibility indicators or tumor markers for anti-cancer agents. The  
 CC gene information for diagnosing prognosis is related to factors similar  
 CC to that for N-myc and TRK genes.  
 XX  
 SO Sequence 777 BP; 249 A; 143 C; 126 G; 256 T; 3 others.  
 Query Match 17.1%; Score 576.8; DP 22; Length 777;  
 Best Local Similarity 94.6%; Pred. No. 5,26-131;  
 Matches 695; Conservative 0; Mismatches 28; Indels 12; Gaps 9;

DB 617 -CAGAAAGGACGTCACATCAAA-GGAGCGTTGGAGAAATGCAATTCATGATG-TC 561  
 QY 2804 AATAGAAATTTGTGTATGAAAGATGGCGACAAAGTGTAAATTTGTGCAAAAACAAAGC 2863  
 DB 560 AATAAGAAATTTGTGTATGAAAGATGGCGACAAAGTGTAAATTTGTGCAAAAACAAAGC 501  
 QY 2864 CAGCAACAAATAATGAGTTGTGAAACAGGAGCTTAAATGAGATTCATATATAAAT 2923  
 DB 509 CAGCAACAAATAATGAGTTGTGAAACAGGAGCTTAAATGAGATTCATATATAAAT 441  
 QY 2924 ATGTACATATATTTGATGATTAAGTAACTATCAATATATGATTTTATGATATAG 2983  
 DB 440 ATG-ACATATATATTTGATGATTAAGTAACTATCAATATATGATTTTATGATATAG 382  
 QY 2984 GTTGTGTTTGTGTGGTGAAGCTTAAATTCACAGGCTATGATATTTTAAATTCATT 3043  
 DB 381 GTTGTGTTTGTGTGGTGAAGCTTAAATTCACAGGCTATGATATTTTAAATTCATT 322  
 QY 3044 AAGTGTATTTGACGTTTAAATGTACCTTGAGAAATAGTTTGTGATATGATTTTGT 3103  
 DB 321 AAGTGTATTTGACGTTTAAATGTACCTTTAGAAATAGCTTGTGCAATGATTTTGT 262  
 QY 3104 TGTGTAAATATTTTGTGCTGATTTTGTATTTTGTATTTTGTATTTTGTATTTT 3163  
 DB 291 TGTGTAAATATTTTGTGCTGATTTTGTATTTTGTATTTTGTATTTTGTATTTT 292  
 QY 3164 AATATTAATGTACAGATGTCAGT-AAAAAAAATATGCTTGAGAAATTAATATATGAA 3222  
 DB 291 AATATTAATGTACAGATGTCAGT-AAAAAAAATATGCTTGAGAAATTAATATATGAA 3142  
 QY 3223 AATTTTACGTTTGTGTGTGACGACATCTT-CTGTGATGCTTAAGTTTAAAGTTTCA 3281  
 DB 141 AATTTTACGTTTGTGTGTGACGACATCTT-CTGTGATGCTTAAGTTTAAAGTTTCA 82  
 QY 3282 TACACATTTTGTGTGTGACGACATCTT-CTGTGATGCTTAAGTTTAAAGTTTCA 3341  
 DB 81 TACACATTTTGTGTGTGACGACATCTT-CTGTGATGCTTAAGTTTAAAGTTTCA 22  
 QY 3342 ATTCAATAAAAAAA 3356  
 DB 21 ATTCAATAAAAAAA 7

Search completed: October 29, 2002, 19:03:44  
 Job time: 584 secs